

DT 24-MAR-1998 (first entry) Multi-epitope peptide used as immunotherapeutic agent #2.
 DE Multi-epitope peptide; immunotherapeutic agent; allergic disease;
 KW T-cell epitope region; allergen; lymphocyte; immunoglobulin E.
 OS Synthetic.
 PN WO9732600-A1.
 PD 12-SEP-1997; J00740.
 PF 10-MAR-1997; JP-080702.
 PR (MEIP) MEIJI MILK PROD CO LTD.
 PA Dairiki K, Iwama A, Kino K, Kume A, Sone T;
 CC WPI; 97-470495/43. Peptide immunotherapeutic agent to treat allergic diseases -
 PT contains multi-epitope peptide containing T cell epitope regions
 PT from different allergens
 PS Claim 6; Page 31; 58pp; Japanese.
 CC The present sequence represents a multi-epitope peptide which is used as
 a new immunotherapeutic agent. It comprises T cell epitope regions from 2
 CC or more different allergens (preferably linked via arginine or lysine
 CC dimers), where the T cell epitope regions have a positivity index
 CC greater than 100 as measured in a patient group responding to the
 CC allergen; have at least 70% reactivity with lymphocytes from patients
 CC responding to the allergen, and are not reactive with immunoglobulin E
 CC (IgE) antibodies from patients responsive to the allergen. The agent can
 CC be used to prevent and treat a wide variety of allergic diseases, e.g. by
 CC desensitisation. Side effects, e.g. those mediated by IgE, are reduced.
 SQ Sequence 105 AA;

Query Match 65.4%; Score 372; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.34e-25; Mismatches 0; Indels 0; Gaps 0;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKVTVAFNQFGNRVFIKRVSNIHGRRIDIFASKNFKHQNTIGRR 51
 QY 1 MKVTVAFNQFGNRVFIKRVSNIHGRRIDIFASKNFKHQNTIGRR 51

RESULT 3

ID W27371 standard; Peptide; 134 AA.

AC W27371;

DT 24-MAR-1998 (first entry)

DE Multi-epitope peptide used as immunotherapeutic agent #3.
 KW Multi-epitope peptide; immunotherapeutic agent; allergic disease;
 T-cell epitope region; allergen; lymphocyte; immunoglobulin E.

OS Synthetic.

PN WO9732600-A1.

PD 12-SEP-1997;

PF 10-MAR-1997; JP-080702.

PR (MEIP) MEIJI MILK PROD CO LTD.

PA Dairiki K, Iwama A, Kino K, Kume A, Sone T;

CC WPI; 97-470495/43. Peptide immunotherapy agent to treat allergic diseases -
 PT contains multi-epitope peptide containing T cell epitope regions
 PT from different allergens
 PS Claim 6; Page 32; 58pp; Japanese.

The present sequence represents a multi-epitope peptide which is used as
 a new immunotherapeutic agent. It comprises T cell epitope regions from 2
 or more different allergens (preferably linked via arginine or lysine
 dimers), where the T cell epitope regions have a positivity index
 greater than 100 as measured in a patient group responding to the
 allergen; have at least 70% reactivity with lymphocytes from patients
 responding to the allergen; and are not reactive with immunoglobulin E
 (IgE) antibodies from patients responsive to the allergen. The agent can
 be used to prevent and treat a wide variety of allergic diseases, e.g. by
 desensitisation. Side effects, e.g. those mediated by IgE, are reduced.
 SQ Sequence 134 AA;

Query Match 65.4%; Score 372; DB 1; Length 134;

Best Local Similarity 100.0%; Pred. No. 1.34e-25; Mismatches 0; Indels 0; Gaps 0;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKVTVAFNQFGNRVFIKRVSNIHGRRIDIFASKNFKHQNTIGRR 51
 QY 1 MKVTVAFNQFGNRVFIKRVSNIHGRRIDIFASKNFKHQNTIGRR 51

Query Match 22.7%; Score 129; DB 1; Length 460;
 Best Local Similarity 100.0%; Pred. No. 6.23e-03; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 182 IDIFASKNFKHQNTIGG 200
 QY 31 IDIFASKNFKHQNTIGG 49

RESULT 5

ID R53690 standard; Protein; 514 AA.

AC R53690;

DT 01-FEB-1995 (first entry)

DE Japanese cedar pollen allergen Cry j II.

KW Cedar pollinos; diagnostic.

OS Cryptomeria Japonica.

PN WO911512-A.

PD 26-MAY-1994.

PR 12-NOV-1992; US-975179.

PT (IMMU-) IMMULOGIC PHARM CORP.

PA Brauer A, Kuo M, Pollock J, Young S;

DR WPI; 94-183513/22.

DR N-PSB; Q66048.

PT Allergenic Cry j II protein and fragments from Japanese cedar

PT Pollen - used to diagnose, treat and prevent Japanese cedar

PT pollinos.

PS Claim 2; Fig 4; 89pp; English.

CC The sequence is of a Japanese cedar pollen allergen Cry j

CC II. The protein and its fragments can be used for diagnosis and

CC treatment of Japanese cedar pollinos and to identify similar

CC sequences in other plants.

CC See also R53692.

SQ Sequence 514 AA;

Query Match 22.7%; Score 129; DB 1; Length 514;

Best Local Similarity 100.0%; Pred. No. 6.23e-03; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 IDIFASKNFKHQNTIGG 254

31 IDIFASKNFHLQKNTIGTG 49

ID	R74333	standard; Protein;	514 AA.
AC	R74333;	(first entry)	
DT	01-NOV-1995		
DE	Japanese cedar pollen allergen.		
KW	desensitizer;		
CC	Cryptomeria japonica.		
CC	EP-655500-A.		
CC	PR-31-MAY-1995.		
CC	PF-03-NOV-1994; 308117.		
CC	PR-05-NOV-1993; JP-299151.		
CC	PR-20-DEC-1993; JP-344596.		
CC	PR-27-DEC-1993; JP-346114.		
PA	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.		
PI	Kurimoto M., Namba M., Torigoe K.		
DR	WPI: 95-19588-26.		
DR	N-PDB; 090156.		
PT	New Japanese cedar pollen allergen polypeptide - and DNA coding for:		
PS	useful for treatment and diagnosis of cedar pollen allergy		
CC	Claim 5; Page 26-28; 41pp; English.		
CC	The gene encoding an allergen of Japanese cedar pollen was isolated by PCR amplification using primers based on portions of the allergen protein. The gene was used for recombinant allergen production in E. coli (vector plasmid PKK-223-3).		
CC	E. coli (vector plasmid PKK-223-3).		
CC	Sequence 514 AA;		
QY	Query Match	22.7%; Score 129; DB 1; length 514;	
Db	Best Local Similarity 100.0%; pred. No. 6. 2.3e-03; 0; Mismatches 0; Indels 0; Gaps 0		
QY	31 IDIFASKNFKHLQKNTIGC 254		
RESULT	7		
ID	R3599	standard; Protein; 514 AA.	
AC	R3599;		
DT	16-AUG-1996 (first entry)		
DE	Japan cedar Pollen CRY J II allergen.		
KW	Allergen; epitope; overlapping peptide; Cry j II; cedar pollen; Sugi pollinosis; diagnosis; treatment.		
OS	Cryptomeria japonica.		
FH	Key Location/Qualifiers		
FT	peptide 1..54		
FT	/*label= sig_peptide		
FT	55..514		
FT	/*label= mat_protein		
PN	J08047392-A.		
PD	20-FEB-1996.		
PF	07-NOV-1994; 297840.		
PR	05-NOV-1993; JP-276773.		
PR	26-MAY-1994; JP-134868.		
PA	(MEIPI) MEIJI MILK PROD CO LTD.		
DR	WPI: 95-165249/17.		
DR	N-PSDB; T8102.		
PT	Japan cedar Pollen allergen CRY J II epitope - comprises at least part of specified 460 amino acid protein		
PS	Claim 1, Page 10-11; 17pp; Japanese.		
CC	R3599 is a Japan cedar Pollen CRY J II allergen which is useful in the diagnosis, prevention and treatment of Sugi Pollinosis, the allergic reaction to Japan cedar pollen. Significant regions of epitope derived from a CRY J II antigen-specific T cell line (see R9781-R97960). Amino acids 61-80 (R97808) of the full mature 460 amino acid allergen are the most allergenic sequence 514 AA;		
CC	of the 90 peptides tested.		

Db	Qy	Result	Score	DB 1:	Length	Indels	Gaps
236	IDIFASKNFELQKNITGTC	254	129;	DB 1;	514;	0;	
	31	IDIFASKNFELQKNITGTC	49				
		R69792	standard; Protein;	514 AA.			
		AC	R69792;				
		DT	27-SEP-1995	(first entry)			
		DE	Japonicum allergen.				
		KW	Japonicum allergen; induced histamine release; antiallergic peptide; IGE cross-linking inhibition.				
		OS	Japonicum sp.				
		PN	W09502412-A.				
		PD	26-JAN-1995.				
		PF	15-JUL-1994; J01164.				
		PR	16-JUL-1994; JP-177008.				
		PR	01-SEP-1993; JP-217725.				
		PT	07-APR-1994; JP-059336.				
		PA	(MEIF) MEIJU MILK PROD CO LTD.				
		PI	Kino K, Kohno Y, Komiya N, Sone T;				
		DR	WPI; 95-067159/09.				
		DR	N-FSDB; 084045, Q84046.				
		PT	Peptide antiallergic agent - inhibits cross-linking of allergen with IgE antibody				
		PS	Example 3, Pages 27-28; 46pp; Japanese.				
		CC	Q84045 encodes R69792, Japonicum allergen, from which the antiallergic peptides R69845-R69809 were derived. The peptide's ability to inhibit the cross-linking of an allergen, to an IgE antibody can be used in the prevention and treatment of allergic diseases.				
		CC	Sequence 514 AA;				

	Query Match	Score	DB	Length
	Best Local Similarity	100.0%	Pred.	No. 6,236-0;
Matches	19;	Conservative	Pred.	No. 0;
Indels	0;	Mismatches	0;	Gaps
QY	31	IDIFASKNFHQKNTIGG	254	49
RESULT	9			
ID	R81586	standard; Protein; 514 AA.		
AC	R81586;	(first entry)		
DT	24-MAY-1996			
DE	Cedar pollen allergen A.			
KW	Cedar; Pollen; Allergen; Immunoglobulin E; IgE; T-cell epitope; antibody; Pollinosis; therapy; immunotherapy.			
CC	Cryptomeria Japonica.			
OS	EP 700929-A2.			
PN	PD 13-MAR-1996.			
PP	PR 08-SEP-1995; 306295.			
PR	10-SEP-1994; JP-242137.			
PR	14-JUL-1995; JP-200204.			
PR	14-JUL-1995; JP-200204.			
(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.				
PT	Hino K, Saito S, Taniguchi Y;			
PT	WPI: 96-140976/15.			
RT	New Peptide(s) derived from cedar pollen allergens - activate allergen-specific T-cells, but not allergen-specific IgE antibodies, used for treating cedar pollinosis.			
CC	Synthetic peptides based on portions of cedar pollen allergens A (R81586) and B (R81587) were tested for their ability to activate cedar allergen-specific T-cells, but not allergen-specific IgE antibodies. 6 peptides (R81580-81585) were identified as T-cell epitopes. These peptides plus subsequences containing			

Db 1 DIFASKNFHQKNTIGT 17
 ID ||||||| standard; peptide; 17 AA.
 AC W80345;
 QY 32 DIFASKNFHQKNTIGT 48

Db 1 KVDGIIAYQNPASWK 16
 ID :|||||||
 QY 65 RVDGIIAYQNPASWK 80

Search completed: Mon Jun 19 15:54:24 2000

Job time : 9 secs.

RESULT 14
 ID W80345 standard; peptide; 17 AA.
 AC W80345;
 DT 11-JAN-1999 (first entry)
 DE Sugi allergen protein Cry12 derived epitope for T cells.
 KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;
 KW sugi pollinosis; allergic reaction; pollen.
 OS Synthetic.
 PN J10259198-A.
 PD 29-SEP-1998.
 PF 22-DEC-1997; 353448.
 PR 24-DEC-1996; JP-343441.
 PA (HAYB) HAYASHIBARA SEIBURSU KAGAKU.
 PA (SANY) SANKYO CO LTD.
 DR WPI; 98-577037/49.
 PT A linked T cell epitope peptide - used for the treatment of
 sugi-pollinosis

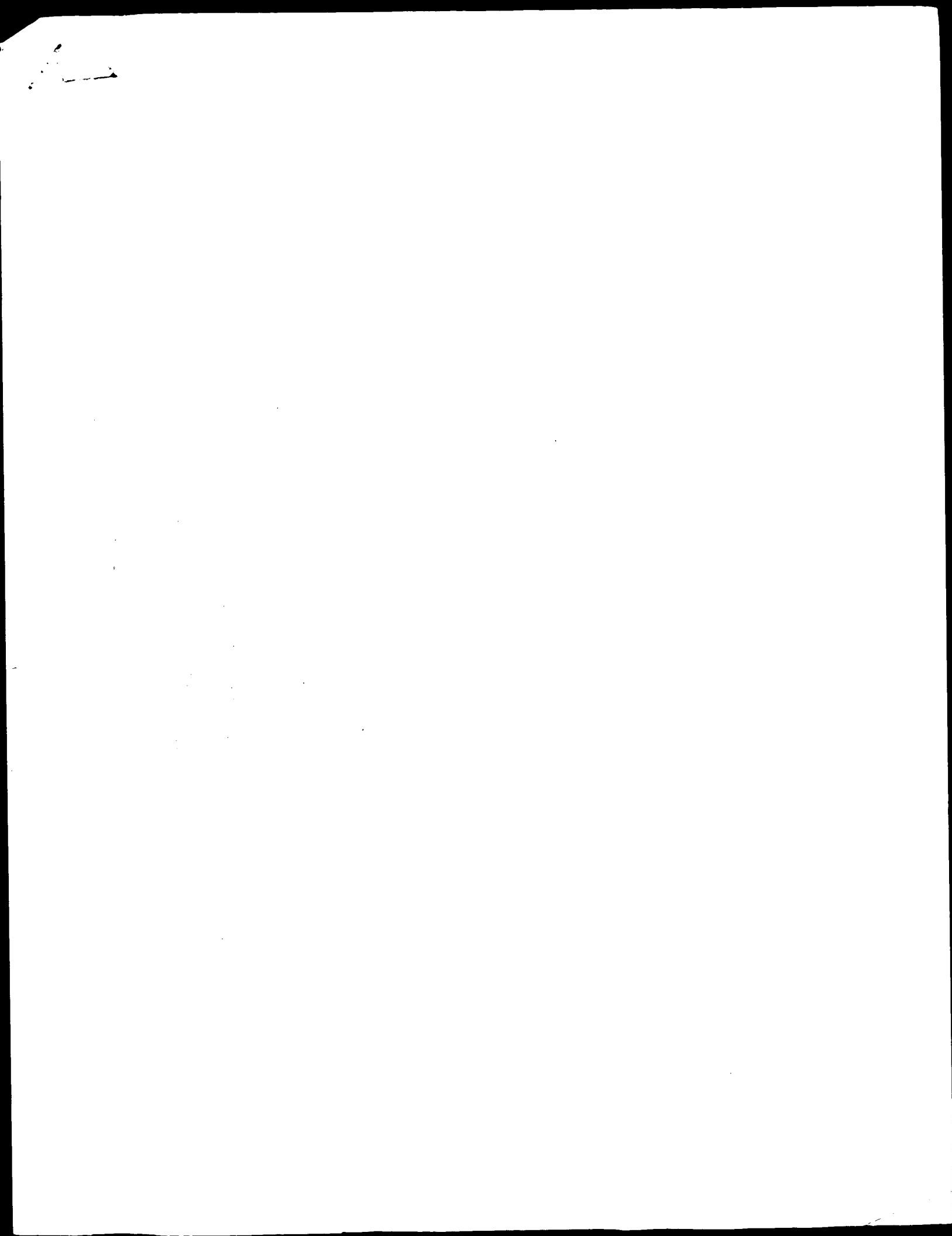
PS Claim 7; Page 18; 21pp; Japanese.
 CC W80339-58 represent epitopes for T cells, derived from the sugi allergen
 proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49
 and W80354-55). The peptides are useful for the treatment of
 sugi-pollinosis, an allergic reaction of the body to pollen.
 Sequence 17 AA;

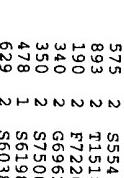
Query Match 19.5%; Score 111; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.03e-01;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 KVDGIIAYQNPASWK 16
 ID :|||||||
 QY 65 RVDGIIAYQNPASWK 80

RESULT 15
 ID R811580 standard; Peptide; 17 AA.
 AC R811580;
 DT 24-MAY-1996 (first entry)
 DE Cedar pollen allergen peptide 8 (T-cell epitope).
 KW Cedar; Cryptomeria Japonica; pollen; allergen; immunoglobulin E;
 IGE; T-cell epitope; antibody; pollinosis; therapy; immunotherapy.
 OS Synthetic.
 PN EP-700920-A2.
 PD 13-MAR-1996.
 PF 08-SEP-1995; 306295.
 PR 10-SEP-1995; JP-242137.
 PR 14-JUL-1995; JP-200221.
 PR 14-JUL-1995; JP-200204.
 PA (HAYB) HAYASHIBARA SEIBURSU KAGAKU.
 PI Hino K, Saito S, Taniguchi Y;
 DR WPI; 96-1140976/15.
 PT New peptide(s) derived from cedar pollen allergens - activate
 PT allergen-specific T-cells, but not allergen-specific IgE antibodies,
 PT used for treating cedar Pollinosis
 PS Claim 4; Page 28; 35pp; English.
 CC Synthetic peptides based on portions of cedar pollen allergens A
 CC (R811586) and B (R811587) were tested for their ability to activate
 CC cedar allergen-specific T-cells, but not allergen-specific IgE
 CC antibodies. 6 Peptides (R811580-R811585) were identified as T-cell
 CC epitopes. These peptides, plus subsequences (R811573-79), essential
 CC for T-cell recognition, and homologous peptides (R811588-96) can
 CC be used as immunotherapeutic agents to treat or prevent cedar
 CC pollinosis, avoiding side-effects such as anaphylaxis.
 SQ Sequence 17 AA;

Query Match 19.5%; Score 111; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.03e-01;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;




 (TM)

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Psrch_pp protein - protein database search, using Smith-Waterman algorithm
 un on: Mon Jun 19 15:53:44 2000; MasPar time 9.04 Seconds
 417.392 Million cell updates/sec
 tabular output not generated.

title: >US-09-142-524A-1
description: (1-80) from US09142524A.Pep
sequence: 569 MKTVAFNOFGPNRRVETKR.....IASRRVDGIIIAAYQNPASWK 80

corecoring table: PAM 150
Gap 11

142080 seqs, 47172405 residues

post-processing: Midlength Match 0%
 Lasting First 45 summaries

database: pir62
 Lpir1 2:pir2 3:pir3 4:pir4

Mean 39.829; Variance 80.867; scale 0.493

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result	entry	title	organism	date
1	JC2498	# type complete		16-Mar-1995 # sequence_revision 12-SEP-1997
		# formal_name Cryptomeia Japonica	# common_name Japanese cedar	
				JC2498; PC2346; A60147
				REFERENCE
		# authors	Komiya, N.; Sone, T.; Shimizu, K.; Morikubo, K.; Kino, K.	
		# journal	Biochem. Biophys. Res. Commun. (1994) 201:1021-1028	
		# title	CDNA cloning and expression of Cry J II, the second major allergen of Japanese cedar Pollen.	
		# cross-references	MURID:94271186	
		# accession	JC2498	
		# molecule_type	mRNA	
		# residues	1-514 # label KOM	
		# cross-references	DBJ:D29772; NID:9506857; PID:a1006734; PID:9506858	
		# accession	PC2346	
		# molecule_type	protein	
		# residues	52-61 # label KO2	
		REFERENCE	A60147	
		# authors	Sakuchi, M.; Inouye, S.; Tanaka, M.; Ando, S.; Usui, M.; Matsumoto, T.	
		# journal	Allergy (1990) 45:309-312	
		# title	Identification of the second major allergen of Japanese cedar pollen.	
		# cross-references	MURID:90342988	
		# accession	A60147	
		# molecule_type	protein	
		# residues	55-64 # label SAK	
		KEYWORDS	glycoprotein; pollen	
		FEATURE	I-54	
		# domain	signal sequence	
		# product	second major allergen Cry J	
		# label	MAT\	
		# label_site	carbohydrate (Asn) (covalent)	
		# predicted		
		SUMMARY		
		# length	514 #molecular_weight	
		# checksum	56583	
		Query	Match	
		# Best_Local_Similarity	22.7%	
		# Score	129	
		# DB	2	
		# length	514	
		# status	Predicted	
		# mismatches	0	
		# indels	0	
		# gaps	0	
		Db	236	IDIFASKNFIQLQKNITGT 254
		Oy	31	IDIFASKNFIQLQKNITGT 49

ALIGNMENTS

CLASSIFICATION #superfamily DNA topoisomerase I
SUMMARY #length 633 #molecular-weight 72694 #checksum 9092

Query Match 17.2%; Score 98; DB 2; Length 633;
 Best Local Similarity 26.5%; Pred. No. 1.40e+01; Indels 3;
 Matches 17; Mismatches 26; Gaps 3;

ENTRY 2

ORGANISM CRY J II protein - Japanese cedar
 #formal_name *Cryptomeria japonica* #common_name Japanese cedar
 #text_change 07-May-1995 #sequence_revision 21-Jul-1995 #text_change
 28-May-1999

ACCESSIONS S48730
 #authors Namba, M.; Kurose, M.; Torigoe, K.; Hino, K.; Taniguchi, Y.;
 Fukuda, S.; Usui, M.; Kurimoto, M.
 FEBs Lett. (1994) 353:124-128
 Molecular cloning of the second major allergen, CRY J II,
 from Japanese cedar pollen.

REFERENCE #journal MNPB:95010777
 #title #cross-references MNPB:95010777

RESULT 2

ENTRY S48730

ORGANISM #status preliminary
 #molecule_type mRNA
 #residues 1-1514 #label NAM
 #cross-references GB:DB37765; NID:9577695; PIDN:BAA07021.1;

SUMMARY #length 514 #molecular-weight 56645 #checksum 586

Query Match 22.7%; Score 129; DB 2; Length 514;
 Best Local Similarity 100.0%; Pred. No. 4.79e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 236 IDIFASKNPHLOKNGTGTG 254
 QY 31 IDIFASKNPHLOKNGTGTG 49

RESULT 3

ENTRY S62737

ORGANISM #type complete
 DNA topoisomerase I - Thermotoga maritima
 #formal_name *Thermotoga maritima*
 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change
 29-Sep-1999 S62737; A72400

ACCESSIONS S62737

REFERENCE #authors Bouthier de la Tour, C.; Kaltoum, H.; Portemer, C.;
 Confalonieri, F.; Hubert, R.; Duguet, M.
 Bi chim. Biophys. Acta (1995) 1264:279-283
 Cloning and sequencing of the gene coding for topoisomerase I
 from the extremely thermophilic eubacterium, *Thermotoga*
maritima. MNPB:9618548

#cross-references MNPB:9618548

RESULT 3

ENTRY S62737

ORGANISM #status Preliminary
 #molecule-type DNA
 #residues 1-633 #label BOU
 #cross-references EMBL:127841; NID:9881493; PIDN:AAA68949.1;
 PID:9881494

REFERENCE #authors Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Nelson, W.C.; Ketchum, K.A.; McDonald, L.; Utterback, T.R.; Malek, J.A.; Linher, K.D.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Heidelberg, J.; Sutton, G.G.; Fleischmann, R.; Fraser, C.M.; Salberberg, S.L.; Smith, H.O.; Venter, J.C.; Fraser, C.M.; Nature (1999) 399:323-329
 Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of *Thermotoga maritima*. MNPB:9287316

#cross-references MNPB:9287316

RESULT 3

ENTRY A72400

ORGANISM #molecule_type DNA
 #residues 1-633 #label ARN
 #cross-references GB:AE001708; GB:AE000512; NID:94980740; PID:94980754; TIGR:TMR258

REFERENCE #genes TM0258

CLASSIFICATION #superfamily DNA topoisomerase I
SUMMARY #length 633 #molecular-weight 72694 #checksum 9092

Query Match 17.2%; Score 98; DB 2; Length 633;
 Best Local Similarity 26.5%; Pred. No. 1.40e+01; Indels 3;
 Matches 17; Mismatches 26; Gaps 3;

ENTRY 4

ORGANISM PRK2 protein - yeast (*Saccharomyces cerevisiae*)
 #formal_name PRK2; protein YNL068c

ACCESSIONS S53913; S59726; S63000; S62996; S58726; S63942

REFERENCE #authors Poehlmann, R.; Philippse, P.
 #text_change 08-Jul-1995 #sequence_revision 01-Sep-1995
 #cross-references S53913

REFERENCE #authors Poehlmann, R.; Philippse, P.
 #text_change 24-Sep-1999 #sequence_revision 01-Sep-1995
 #cross-references S53913; S59726; S63000; S62996; S58726; S63942

REFERENCE #authors Zhu, G.; Davis, T.N.
 #text_change submitted to the EMBL Data Library, January 1995
 #description Two fork head homologs in *S. cerevisiae*.
 #accession S59725

REFERENCE #authors Poehlmann, R.; Philippse, P.
 #text_change submitted to the Protein Sequence Database, April 1996
 #cross-references EMBL:1138850; NID:9623607; PIDN:AAA60339.1;
 #molecule_type DNA
 #residues 1-862 #label POW
 #cross-references EMBL:271344; NID:91301948; PIDN:CA95942.1;
 #molecule_type DNA
 #cross-references EMBL:271344; NID:91301949; MIPS:YNL068C

REFERENCE #authors Berger, P.; Doignon, F.; Crouzet, M.
 #text_change submitted to the Protein Sequence Database, April 1996
 #cross-references EMBL:Z1344; MIPs:YNL068C

REFERENCE #authors Berger, P.; Doignon, F.; Crouzet, M.
 #text_change submitted to the Protein Sequence Database, April 1996
 #cross-references EMBL:Z1344; MIPs:YNL068C

REFERENCE #authors Berger, P.; Doignon, F.; Crouzet, M.
 #text_change yeast (1995) 11:967-974
 #description The sequence of a 44 420 bp fragment located on the left arm
 #title Of chromosome XIV from *Saccharomyces cerevisiae*.
 #cross-references MNPB:96021608

REFERENCE #status nucleic acid sequence not shown; translation not shown
 #molecule_type DNA
 #residues 1-440 #label BER
 #cross-references EMBL:Z1344; MIPs:YNL068C

REFERENCE #status nucleic acid sequence not shown; translation not shown
 #molecule_type DNA
 #residues 1-440 #label BBW
 #cross-references EMBL:U1214; NID:91314216; PIDN:AAA99643.1;
 #note the nucleotide sequence was submitted to the EMBL Data Library, July 1994

REFERENCE #genes TM0258

Poehlmann, R.; Philipsen, P.
 Yeast (1996) 12:31-402
 Sequencing a cosmid clone of *Saccharomyces cerevisiae*
 chromosome XIV reveals 12 new open reading frames (ORFs)
 and an ancient duplication of six ORFs.

#cross-references MUID:96267764
 accession S63942
 #status nucleic acid sequence not shown; translation not shown
 #molecule-type DNA
 #residues 1862 #label POF
 #cross-references EMBL:X8570; NID:9791101; PIDN:CA60193.1;
 PID:9791119
 #note the nucleotide sequence was submitted to the EMBL Data
 Library, April 1995

GENETICS
 #gene SGD:FKH2
 ##cross-references SGD:S0005012; MIPS:YNL068C
 CLASSIFICATION
 #map-position 11L
 #superfamily unassigned fork head proteins; fork head
 DNA-binding domain homology
 FEATURE
 340432 #length 862 #molecular-weight 9434 #checksum 4135
 Query Match Best Local Similarity 17.0%; Score 97; DB 2; Length 862;
 Matches 20; Conservative 23; Mismatches 27; Indels 5; Gaps 5;
 Db 65 AYAKLGLGNWTTVYKDL-EVSI-GRNTDPLNA-ALQNSDGKNSKVNIIDPAKVSR 121
 Qy 6 AFNQF-GNRRVIVIKRVSNVNIIHGRRIDIFASKNFHLQKNTIGTGRRIKLSGKIASR 64
 Db 122 K-HAIKIYKNMTCGG 135
 Qy 65 RVGGIAIAYQNFAFW 79

RESULT 5
 ENTRY D48562 #type complete
 TITLE hypothetical nucleic acid-binding protein - San Miguel sea
 ORGANISM lion virus (serotype 4)
 DATE 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change
 ACCESSIONS D48562
 REFERENCE A48562
 #authors Neill, J. D.
 #journal Virus Res. (1992) 24:211-222
 #title Nucleotide sequence of the capsid protein gene of two
 serotypes of San Miguel sea lion virus: identification of
 conserved and non-conserved amino acid sequences among
 calicivirus capsid proteins.
 #cross-references MUID:92410750
 #accession D48562
 #status preliminary
 #molecule_type genomic RNA
 #residues 1-110 #label NEI
 ##cross-references GB:MB7482; NID:9334886; PID:9334889
 SUMMARY #length 110 #molecular-weight 12566 #checksum 2707
 Query Match Best Local Similarity 16.7%; Score 95; DB 2; Length 110;
 Matches 13; Conservative 17; Mismatches 13; Indels 2; Gaps 2;
 Db 10 FLNSYANAVVEGKGKLDSL-ASKGLOIQLSKRALTERAFVNVLAKER 53
 Qy 17 FIKYVSNVIHGRIDIFASKNFHLQKNTIGTGRISL-KLTSGK 60

RESULT 6
 ENTRY JC2124 #type complete
 TITLE major allergen Cry j I precursor (clone pCCI-15) - Japanese

ORGANISM cedar
 DATE 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change
 ACCESSIONS JC2124
 REFERENCE JC2123
 #authors Sone, T.; Komiya, N.; Shimizu, K.; Kusakabe, T.; Morikubo,
 Biochem. Biophys. Res. Commun. (1994) 199:619-625
 #journal Cloning and sequencing of cDNA coding for Cry j I, a major
 allergen of Japanese cedar pollen.
 #title allergen of Japanese cedar pollen.
 #cross-references MUID:94183234
 #accession JC2124
 #molecule_type mRNA
 #residues 1-374 #label SON
 ##cross-references GB:D21544; NID:9493631; PID:91006086; PID:9493632
 #experimental_source pollen
 #accession PC2065
 #molecule_type protein
 #residues 22-53; 58-81; 219-232; 236-258; 299-307; 346-372 #label S02
 #note the authors described carbohydrate binding site for
 the authors described carbohydrate binding site for
 residue 279
 CLASSIFICATION #superfamily pectate lyase LAT59
 FEATURES
 #superfamily glycoprotein; pollen
 #domain signal sequence #status predicted #label SIG
 #product major allergen Cry j I (clone pCCI-2-2) #status
 #predicted #label MAT
 #binding-site carbohydrate (Asn) (covalent) #status
 #predicted

SUMMARY #length 374 #molecular-weight 40645 #checksum 2920

Query Match Similarity 16.7%; Score 95; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.50e-01; Mismatches 0;
Matches 13; Conservative 0; Indels 0; Gaps 0;

Db 234 MKVYVAFNQFGPN 246
Qy 1 MKVYVAFNQFGPN 13

RESULT 8

ENTRY A40351 #type complete
TITLE adhesion-type protein ADMIX - human
ORGANISM Homo sapiens #common_name man
DATE 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change
20-Mar-1998

ACCESSIONS A40351

REFERENCE Legouis, R.; Hardelin, J.P.; Levilliers, J.; Claverie, J.M.; Compain, S.; Wunderle, V.; Millasseau, P.; Le Paslier, D.; Cohen, D.; Catterina, D.; Bouquellet, L.; Delamare-Van de Waal, H.; Lutfalla, G.; Weissbach, J.; Petit, C.

Cell (1991) 67:423-435

The candidate gene for the X-linked Kallmann syndrome encodes a protein related to adhesion molecules.

#journal #status preliminary

##molecule_type mRNA
##residues 1-679 ##label LEG
##cross-references GB:560085; NID:9237595; PID:9237597

GENETICS

#gene GDB:KALL; KAL

#cross-references GDB:170116; OMIM:308700

CLASSIFICATION #map_position Xp22.32-Xp22.32

FEATURE 129-175

SUMMARY #length 679 #molecular_weight 76301 #checksum 1231

Query Match Similarity 16.7%; Score 95; DB 2; Length 679;
Best Local Similarity 27.1%; Pred. No. 3.50e-01; Mismatches 16; Conservative 19; Indels 1; Gaps 1;

Db 247 VOLDIPIRSRWYQFRVAVNVHGTGFTTASBSKKHFRSSKDSAPPAPANRLANSVNS 304
Qy 5 VAFNQFGPNRRYVFKRVSNLVIGRRRIDFASKNFHQLNKTIGGRRIKLTSKIAS 63

RESULT 9

ENTRY S17982 #type complete
TITLE Kallmann syndrome protein KALIG-1 - human
ORGANISM Homo sapiens #common_name man
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
19-Feb-1999

ACCESSIONS S17982

REFERENCE Franco, B.; Guidoli, S.; Pragliola, A.; Incerti, B.; Bardon, M.; Tonlorenzi, R.; Carrozzo, R.; Maestrini, E.; Pieretti, M.; Tailor-Miller, P.; Brown, C.J.; Willard, H.F.; Lawrence, C.; Persico, M.G.; Camerino, G.; Ballabio, A.

Nature (1991) 333:529-536

A gene deleted in Kallmann's syndrome shares homology with neural cell adhesion and axonal path-finding molecules.

#cross-references MURD:92018217
#accession S17982

#status preliminary

##molecule_type mRNA
##residues 1-680 ##label FRA
##cross-references EMBL:X60299; NID:934024; PID:934025

GENETICS

#journal #title

##cross-references GDB:120116; OMIM:308700
##map_position Xp22.32-Xp22.32

RESULT 10

ENTRY S55415 #type complete
TITLE ATP-binding transport protein ywja - Bacillus subtilis
ORGANISM ABC transporter (ATP-binding protein) ywja
#formal_name Bacillus subtilis
DATE 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change
20-Sep-1999

ACCESSIONS S55415; G70059

REFERENCE Glaser, P.; Danchin, A.

#authors submitted to the EMBL data Library, May 1995
#submission Cloning and Sequencing of the *Bacillus subtilis* chromosomal region from 320 degrees to 321 degrees.

#accession S55415

##molecule_type DNA
##residues 1-575 ##label GLA
##cross-references EMBL:249792; NID:9853752; PID:CAA89862.1;
PID:9853754

REFERENCE A69580

#authors Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azereedo, V.; Bertino, M.G.; Bessieres, P.; Boilotin, A.; Borchart, S.; Bertois, R.; Bourstier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, J.J.; Conerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fakret, C.; Ferrari, E.; Fouger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleon, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.; Guisseppi, G.; Guy, B.J.; Haga, B.; Hailech, J.; Harwood, C.R.; Henaut, A.; Hilpert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamoto, D.; Kasahara, Y.; Klaerr-Blanchard, A.; Klein, S.; Kobayashi, T.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Oigawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Porwolk, S.; Prescott, G.A.M.; Prosecan, E.; Puig, P.; Pur nelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.; Schleicher, S.; Schroeter, R.; Sofcone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.S.J.; Serror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takashashi, H.; Takemaru, K.; Takeichi, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, P.; Togoni, A.; Tosato, V.; Uchiyama, S.; Vandembol, M.; Vanner, F.; Vassarotti, A.; Viari, A.; Wambutt, R.; Wedler, E.; Weitzenegger, H.; Wittenberg, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshikawa, H.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

#journal #title

Nature (1997) 390:249-256

The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

#accession -G70059

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#status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-575 #label KUN
##cross-references GB:299123; GB:AL009126; NID:g2636240;
            PID:NCAB15751_1; PID:e118624; PID:g2636260
GENETICS
#gene YWIA
#start_codon GRG
CLASSIFICATION #superfamily unassigned ATP-binding cassette proteins;
KEYWORDS ATP; P-loop
FEATURE 349-543
SUMMARY #domain ATP-binding cassette homology #label ABC\ATP-binding cassette homology #molecular-weight 64562 #checksum 4403
Query Match Best Local Similarity 29 2%; Pred. No. 4.73e-01; Length 575; Matches 19; Conservative 17; Mismatches 27; Indels 2; Gaps 2;
Db 176 KKKTKAFTLNLKQDGDFARVENNIGGIRLYAFGNFAFEKERRFAVNQNRRTV-KLSSY 234
Qy 1 MKTVIAFWQFGPRRVRVFKRVSNIHLQRDIFASKRNFHQLQNTGTGR-RISKLTS 59
Db 235 KIMAK 239
Qy 60 KIASR 64

RESULT 11
ENTRY T15183 #type complete
TITLE hypothetical protein C18B3.3 - Caenorhabditis elegans
ORGANISM #formal_name Caenorhabditis elegans
DATE 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
ACCESSIONS
REFERENCE
#authors Connell, M.; Maggi, L.
#submission submitted to the EMBL Data Library, April 1997
#accession T15183
#status preliminary; translated from GB/EMBL/DBJ
##cross-references EMBL:AF00265; NID:91947147; PID:91947148; PID:AB52941_1; GSDB:GN00019; CBSP:C18E3..3
GENETICS
#gene CESP:C18E3..3
#molecule_type DNA
#experimental_source strain Bristol N2; clone C18E3

RESULT 13
ENTRY A69628
TITLE G669628 #type complete
ORGANISM #formal_name Bacillus subtilis
DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
1-Jun-1999
ACCESSIONS
REFERENCE
#authors Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertolo, M.G.; Bessieres, P.; Boilotin, A.; Borecht, S.; Boriss, R.; Bourrier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, J.J.; Conerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.; Erlich, S.D.; Ellmerer, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Fouger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleton, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Goilait, E.J.; Grandi, G.; Guiseppi, G.; Guy, B.J.; Haga, K.; Haichach, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi, T.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Laarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maaueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogiara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portelle, D.; Porwollik, S.; Prescott, A.M.; Presecan, E.; Puicic, P.; Purelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Seiror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Tagagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.;
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F72207 #type complete

riboflavin synthase, alpha subunit - Thermotoga maritima (strain MSB8)

#formal-name Thermotoga maritima

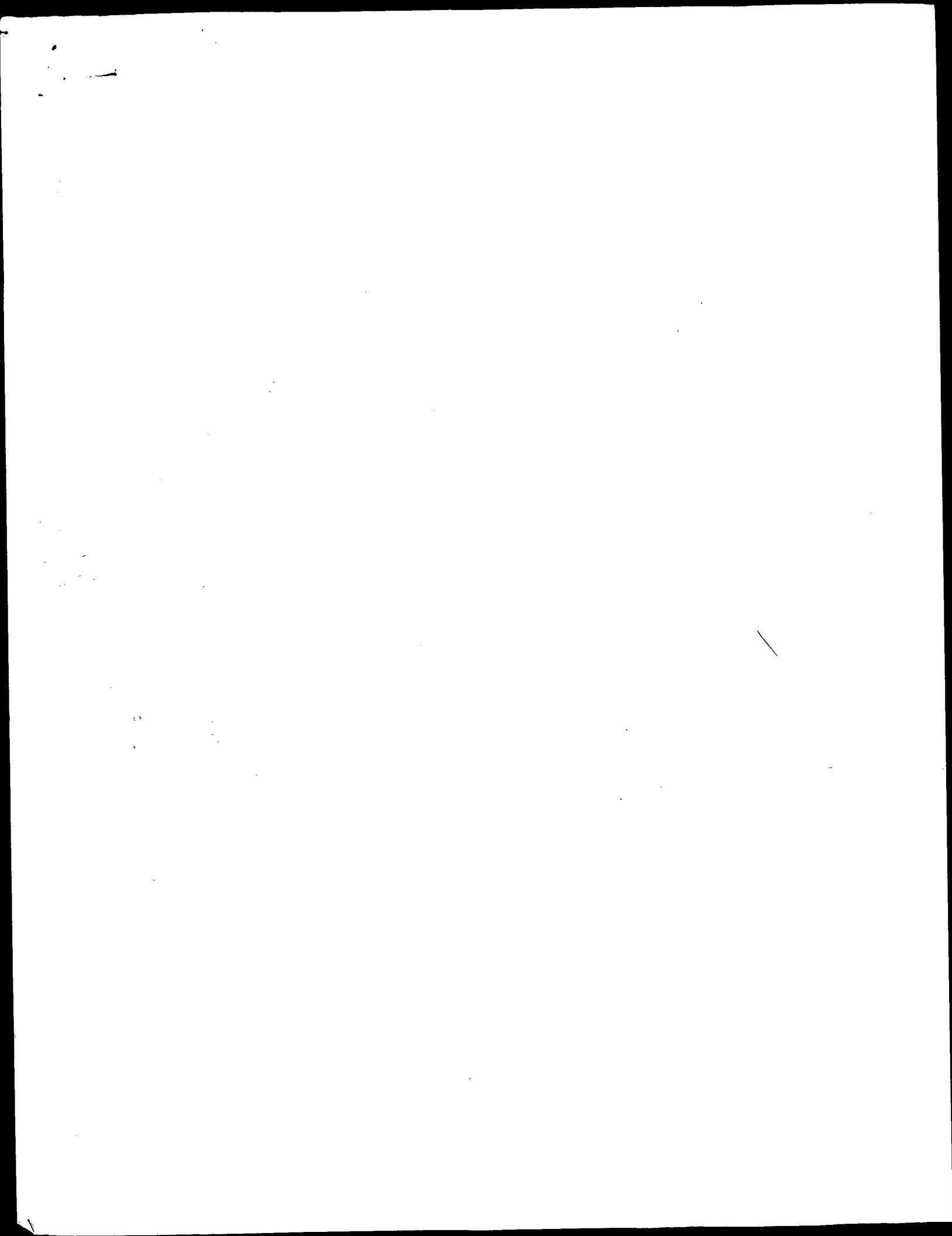
11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change

Wed Jun 21 09:22:48 2000

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Page 7

joy time : 14 secs.



CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-- SUBUNIT: MONOMER (BY SIMILARITY).
CC	-- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK. IN WHICH A TYROSYL OXYGEN IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
CC	-- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE FAMILY.
CC	-- This SWISS-PROT entry is copyright. It is produced through a collaboration between the European Bioinformatics Institute. There are no restrictions on use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-- AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
DR	PROSTINE; PS00362; POLYGALACTURONASE; 1.
DR	PFAIM; PF00095; Glyco_hydro_28; 1.
KW	Hydrolyase; Glycosidase; Cell wall; Signal; Zymogen; Fruit ripening; Amylopaste; Glycoprotein; Allergen.
FT	SIGNAL 1 ?
FT	PROPEP ?
FT	CHAIN 46 433
FT	PROPEP 434 514
FT	ACT_SITE 278 278
FT	CARBONID 460 460
FT	CARBONID 472 472
FT	CONFLICT 12 15
FT	CONFLICT 12 12
FT	CONFLICT 34 35
FT	CONFLICT 37 37
FT	CONFLICT 88 88
FT	CONFLICT 98 98
FT	CONFLICT 451 451
FT	CONFLICT 454 454
FT	CONFLICT 504 504
FT	CONFLICT 507 507
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SQ	Query Match 22.7%; Score 129; DB 1; Length 514; Best Local Similarity 100.0%; Pred. No. 3.32e-07; Matches 0; Mismatches 0; Indels 0; Gaps 0;
Db	236 IDIFASKNHFHQKNTIGG 254 49
Qy	31. IDIFASKNHFHQKNTIGG 49
RESULT 2	TOP1_THEME STANDARD; PRT: 633 AA.
ID	P46799; 01-NOV-1995 (Rel. 32, Created)
DT	01-NOV-1995 (Rel. 32, Last sequence update)
DT	15-FEB-2000 (Rel. 39, Last annotation update)
DE	DNA TOPOISOMERASE I (EC 5.99.1.2) (OMEGA-PROTEIN) (RELAXING ENZYME)
DE	(UNTWISTING ENZYME) (SWIVELASE).
GN	TOPA OR TM0258.
OS	Thermotoga maritima.
OC	Bacteria; Thermotogales; Thermotoga.
[1]	SEQUENCE FROM N.A.
RN	SEQUENCE FROM D.M. 3109;
RC	STRAIN=MBB / MEDLINE: 96130548.
RX	MEDLINE: 96130548.
RX	Boutinier de la Tour C., Kaltoum H., Portemer C., Confalonieri F.,
RA	Huber R., Duguet M.,
RT	"Cloning and sequencing of the gene coding for topoisomerase I from the extremely thermophilic eubacterium, <i>Thermotoga maritima</i> .";
RL	Biochim. Biophys. Acta 1264:279-283(1995).
RN	SEQUENCE FROM N.A.
[2]	SEQUENCE FROM N.A.
RX	SEQUENCE FROM N.A.
RC	STRAIN=MSB8 / DSM 3109;
RX	STRAIN=MSB8 / MEDLINE: 99287316.
RA	Nelson K.E., Clayton R.A., Gill S.R., Ginn M.L., Dodson R.J., Haft D.H., Hickie E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RX	"Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of <i>Thermotoga maritima</i> .";
RL	Nature 399:323-329(1999).
RX	-- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.
CC	- - CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED
CC	-- DNA, FOLLOWED BY PASSAGE AND REJOINING.
CC	-- SUBUNIT: MONOMER (BY SIMILARITY).
CC	-- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK. IN WHICH A TYROSYL OXYGEN IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
CC	-- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE FAMILY.
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CC	-- AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
DR	PROSTINE; PS00362; POLYGALACTURONASE; 1.
DR	PFAIM; PF00095; Glyco_hydro_28; 1.
KW	Hydrolyase; Glycosidase; Cell wall; Signal; Zymogen; Fruit ripening; Amylopaste; Glycoprotein; Allergen.
FT	SIGNAL 1 ?
FT	PROPEP ?
FT	CHAIN 46 433
FT	PROPEP 434 514
FT	ACT_SITE 278 278
FT	CARBONID 460 460
FT	CARBONID 472 472
FT	CONFLICT 12 15
FT	CONFLICT 12 12
FT	CONFLICT 34 35
FT	CONFLICT 37 37
FT	CONFLICT 88 88
FT	CONFLICT 98 98
FT	CONFLICT 451 451
FT	CONFLICT 454 454
FT	CONFLICT 504 504
FT	CONFLICT 507 507
FT	SEQUENCE 514 AA: 56645 MW: 624611C3CFR8D6302 CRC64;
SQ	Query Match 22.7%; Score 129; DB 1; Length 514; Best Local Similarity 100.0%; Pred. No. 3.32e-07; Matches 0; Mismatches 0; Indels 0; Gaps 0;
Db	236 IDIFASKNHFHQKNTIGG 254 49
Qy	31. IDIFASKNHFHQKNTIGG 49
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ID	P1813; 01-NOV-1995 (Rel. 32, Created)
DT	01-NOV-1995 (Rel. 32, Last sequence update)
DT	15-DEC-1998 (Rel. 37, Last annotation update)
DE	FORK HEAD PROTEIN HOMOLOG 2.
GN	KH2 OR YNL068C OR N2403 OR YNL2403C.
OS	Saccharomyces cerevisiae (Baker's yeast), Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Saccharomycetes; Saccharomycetales; OC
RN	SEQUENCE FROM N.A.
RX	SEQUENCE FROM N.A.
RC	STRAIN=S288C: MEDLINE: 99287316.
RX	SEQUENCE FROM N.A.
RN	SEQUENCE FROM N.A.
RX	SEQUENCE FROM N.A.
RA	Ihu G., Davis T.N.; Submitted (XXX-1995) to the EMBL/GenBank/DDBJ databases.
RN	[2]
RX	SEQUENCE FROM N.A.
RA	Ihu G., Davis T.N.; Submitted (XXX-1995) to the EMBL/GenBank/DDBJ databases.
RN	[2]
RX	SEQUENCE FROM N.A.
RA	STRAIN=S288C / FY1679; MEDLINE: 96267764.
RX	SEQUENCE FROM N.A.
RA	Poelmann R., Philippsen P.; "Sequencing a cosmid clone of <i>Saccharomyces cerevisiae</i> chromosome XIV reveals 12 new open reading frames (ORFs) and an ancient duplication of six ORFs.";
RX	least 12.391-402(1996).
RN	[3]
RX	SEQUENCE OF 1-440 FROM N.A.
RC	STRAIN=S288C / FY1676; MEDLINE: 96021608.
RX	Berrezi P., Dolognon G., Crouzet M.; "The sequence of a 44-420 bp fragment located on the left arm of chromosome XIV from <i>Saccharomyces cerevisiae</i> .";

Db 95 LTAQQRAN-IELTFERCAA 112
 ||::| : | ::| : |:
 60 KIASRRYDGILAYONAS 78
 Qy

RESULT 15 STANDARD; PRT; 394 AA.

ID IJ51_YEAST
 AC P4127;
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE HYPOTHETICAL 44.4 KD PROTEIN IN MIRI-STE18 INTERGENIC REGION.

GN YJ081C OR J1847.
 OS Saccharomyces cerevisiae (Baker's Yeast)
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN [1]

RN SEQUENCE FROM N.A.

RP STRAIN=S88C;

RX MEDLINE: 96417976.

RA Huang M.-B., Manusz V., Chuat J.-C., Galibert F.; reveals 36 open
 RT reading frames and a gene cluster with a counterpart on chromosome
 RI XI."

RL Yeast 12:869-875(1996).

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 CC or send an email to license@isb-sib.ch).

CC DR EMBL: Z49578; CAA89608.1; -.
 DR EMBL: L47993; AAB3904.1; -.
 KW Hypothetical protein
 SEQUENCE 394 AA; 44427 MW; 4359DD8A4C8AA230 CRC64;

Query Match 14.9% Score 85; DB 1; Length 394;
 Best Local Similarity 29.8%; Pred. No. 2.10e+00;
 Matches 14; Conservative 15; Mismatches 17; Indels 1; Gaps 1;

Db 102 RSFKSSLFHRTIGSYLELLAAPNQTSRPFDSRSLSVNLNTGK 148
 || : : || : || : || : | : || : | : || : | : || : |:
 Qy 15 RVFIKRYSNVTHGRRIDFASKRFILQKNGITGRIS-LKLISGK 60

Search completed: Mon Jun 19 15:52:50 2000
 Job time : 10 secs.

KW: Hydrolase; Transmembrane; Phosphorylation; ATP-binding.
 FT: MOD-RES 442 442 PHOSPHORYLATION (PROBABLE).
 SEQUENCE 1160 AA; 130984 MW; 68G09A2D CRC32;

Query Match, Best Local Similarity 26.8%; Score 91; DB 5; Length 1160; Matches 15; Conservative 16; Mismatches 22; Indels 3; Gaps 3; Qy 1 MKVTVAFNQPG-PNRFVFKRVSNTIH-RRIDFASKNFHQ-KNTGTGRIS 53

RESULT 6 ID Q9X2E7 PRELIMINARY; PRT; 190 AA.

ID DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DE RIBOLAVIN SYNTHASE, ALPHA SUBUNIT.
 GN TM1827.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogales; Thermotoga.
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE; 99287316.
 RA NELSON K. E., CLAYTON R. A., GILL S. R., GWYNN M. L., DODSON R. J.,
 RA HAFT D. H., HICKEY E. K., PETERSON J. D., NELSON W. C., KETCHUM K. A.,
 RA McDONALD L., UTTERBACK T. R., MALEK J. A., LINHER K. D., GARRETT M. M.,
 RA STEWART A. M., COTTON M. D., PRATT M. S., PHILLIPS C. A., RICHARDSON D.,
 RA HEIDELBERG J., SUTTON G. G., FLEISCHMANN R. D., WHITE O., SALZBERG S. L.,
 RA SMITH H. O., VENTER J. C., FRASER C. M.;
 RT "Evidence for lateral gene transfer between Archaea and bacteria from genome sequence of *Thermotoga maritima*.";
 RL Nature 399:323-325(1999).
 RN [2]
 SEQUENCE FROM N.A.
 RA NELSON K. E., CLAYTON R. A., GILL S. R., GWYNN M. L., DODSON R. J.,
 RA HAFT D. H., HICKEY E. K., PETERSON J. D., NELSON W. C., KETCHUM K. A.,
 RA McDONALD L., UTTERBACK T. R., MALEK J. A., LINHER K. D., GARRETT M. M.,
 RA STEWART A. M., COTTON M. D., PRATT M. S., PHILLIPS C. A., RICHARDSON D.,
 RA HEIDELBERG J., SUTTON G. G., FLEISCHMANN R. D., WHITE O., SALZBERG S. L.,
 RA SMITH H. O., VENTER J. C., FRASER C. M.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AAC001819; AAD36890.1; -.
 SQ SEQUENCE 190 AA; 21678 MW; F999479B CRC32;

Query Match, Best Local Similarity 28.6%; Score 89; DB 2; Length 190; Matches 10; Conservative 13; Mismatches 11; Indels 1; Gaps 1; Qy 60 RRTNLWFSRFYNEK-SLAGSRVVEGHLYVHGD 93

RESULT 7 ID Q09783 PRELIMINARY; PRT; 108 AA.

ID AC 009783
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE CAPSID.
 OS San Miguel sea lion virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Calicivirus.
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=SMSV-17;
 RX MEDLINE; 98187296.
 RA MATSON D. O., BERKE T., DINULOS M. B., POET S. E., ZHONG W. M., DAI X. M.,
 RA JIANG X., GOLDING B., SMITH A. W.;
 RT "Partial characterization of the genome of nine animal

RESULT 8 ID P73865 PRELIMINARY; PRT; 350 AA.

ID DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
 DE SENSOR TRANSDUCTION HISTIDINE KINASE.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC6803;
 RA TABATA S.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=PCC6803;
 RA MEDLINE; 97061201.
 RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
 RA MIYAMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
 RA HOSOCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARIO K., OKUMURA S.,
 RA SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
 RA TABATA S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
 RT DNA Res. 3:105-136(1996).
 RL DR EMBL; D99910; BAA7927.1; -.
 DR PFAM; PF00512; signal_1;
 SQ SEQUENCE 350 AA; 39445 MW; EEEFE2A0B CRC32;

Query Match, Best Local Similarity 38.6%; Score 88; DB 2; Length 350; Matches 17; Conservative 12; Mismatches 11; Indels 4; Gaps 2; Qy 29 RRDIFSKNHLQKNGTGRISLKTSKIAS 63

RESULT 9 ID P89682 PRELIMINARY; PRT; 110 AA.

ID AC P89682;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE CASPID PROTEIN.
 OS Vesicular exanthema of swine virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Calicivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=48;
 RA NEILL J. D., MEYER R. F., SEAL B. S.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U76874; AAC13800.1; -.
 SQ SEQUENCE 110 AA; 12649 MW; 2998BB44B CRC32;

Query Match, Best Local Similarity 35.3%; Score 88; DB 14; Length 110; Matches 12; Conservative 12; Mismatches 9; Indels 1; Gaps 1; Qy 17 FIKRVSNVITIAGCKKL-ASKGLQKLNRAALDTER 42

RESULT 10 ID 10 FLNGVANAAIEKKKL-ASKGLQKLNRAALDTER 42 PRE. No. 4 65e-01; Mismatches 22; Indels 3; Gaps 3; Qy 17 FIKRVSNVITIAGCKKL-ASKGLQKLNRAALDTER 42

RT calciviruses;"
 RL Arch. virol. 141:2443-2456(1996).
 DR EMBL; U52005; AAC57041.1;
 SQ SEQUENCE 108 AA; 12354 MW; 476A3E95 CRC32;

Query Match, Best Local Similarity 35.3%; Score 88; DB 14; Length 108; Matches 12; Conservative 12; Mismatches 9; Indels 1; Gaps 1; Qy 17 FIKRVSNVITIAGCKKL-ASKGLQKLNRAALDTER 42

Best local similarity 28.6%; Pred. No. 1.71e+00; Mismatches 11; Indels 2; Gaps 2; Matches 12; Conservative 17; Mismatches 11; Indels 2; Gaps 2; Matches 12; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

Db 10 FLNSVANAAVEGKKLDL-ASRGQLQLRSALDERDFNYAKLA 50
Qy 17 FIKRVSNVIHGRIDIFASKNHFQKNTIGRRIISL-KLT 57

RESULT 10 PRELIMINARY; PRT; 394 AA.
ID 065457
AC 065457;
DT 01-AUG-1998 (TREMBREL. 07, Last sequence update)
DT 01-AUG-1998 (TREMBREL. 07, Last annotation update)
DE PECTATE LYASE LIKE PROTEIN.
GN FIN20_190
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; euphyllophytes; Spermatophytina; Magnoliophytina; eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC [1]
RN SEQUENCE FROM N.A.
RP BEVAN M., WEDLER H., WAMBUTT R., BANCROFT I., MEWES H.W., MAYER K., RA SCHUELLER C.; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU ARABIDOPSIS SEQUENCING PROJECT;
RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL02140; CAA8112.1;
DR MENDEL; 29068; Arath; 1088; 29068.
DR PFAM; PF00544; Pectinase; 1.
DR PRINTS; PR00807; AMBALERGEN.
KW Lyase.
SQ 394 AA; 43299 MW; 8B9A93C9 CRC32;

Query Match 15.3%; Score 87; DB 10; Length 394;
Best Local Similarity 91.7%; Pred. No. 1.71e+00;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

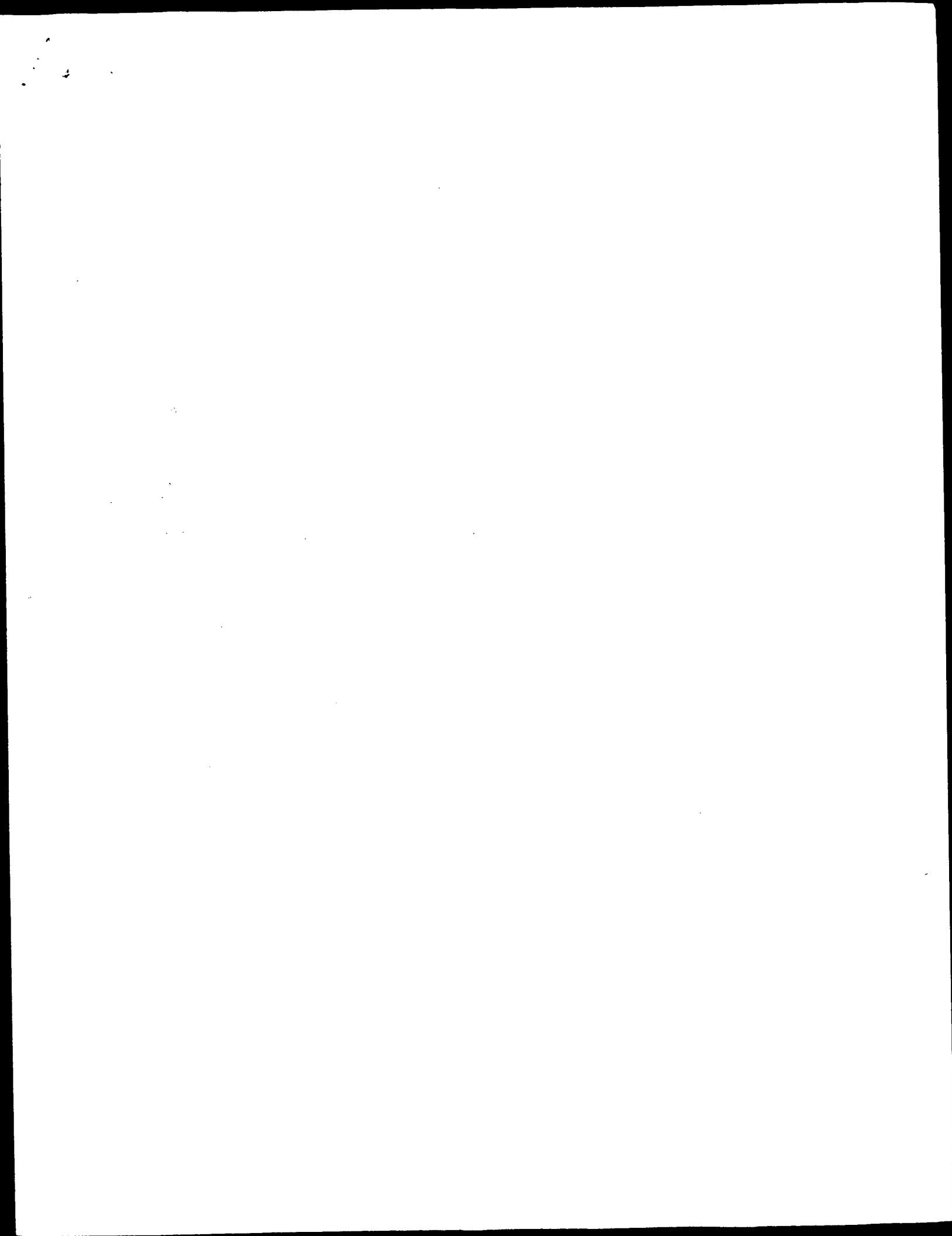
Db 256 MKVTVAHNHFGP 267
Qy 1 MKVTVAFNQFGP 12

RESULT 11 PRELIMINARY; PRT; 394 AA.
ID 055456
AC 055456;
DT 01-AUG-1998 (TREMBREL. 07, Created)
DT 01-AUG-1998 (TREMBREL. 07, Last sequence update)
DT 01-NOV-1999 (TREMBREL. 12, Last annotation update)
DE PECTATE LYASE LIKE PROTEIN.
GN FIN20_180
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophytina; Embryophytina; euphyllophytes; Spermatophytina; Magnoliophytina; eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC [1]
RN SEQUENCE FROM N.A.
RP BEVAN M., WEDLER H., WAMBUTT R., BANCROFT I., MEWES H.W., MAYER K., RA SCHUELLER C.; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA WATERSTON R.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RL WATERSTON R.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF036673; AAB88336.1; -.
SQ SEQUENCE 478 AA; 55107 MW; AC660609 CRC32;

Query Match 15.3%; Score 87; DB 5; Length 478;
Best Local Similarity 22.9%; Pred. No. 1.71e+00;
Matches 11; Conservative 20; Mismatches 15; Indels 2; Gaps 2;

Db 207 IQVKTALKSFQPTPRNFYEHIGFIVTNRAKLN-VGKDLIFQNLFG 253
Qy 1 MKVTVAFNQFGPNRRVFKRVSNIHGR-RIDIFASKNHFQKNTIG 47

RESULT 13 PRELIMINARY; PRT; 440 AA.
ID 069651
AC 069651;
DT 01-AUG-1998 (TREMBREL. 07, Created)
DT 01-AUG-1998 (TREMBREL. 07, Last sequence update)
DT 01-NOV-1998 (TREMBREL. 08, Last annotation update)
DE HYPOTHETICAL 47.7 KD PROTEIN.
GN MTV025_041.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinomycetinae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OC [1]
RN



CC and W80354-55). The peptides are useful for the treatment of sugi-pollinosis, an allergic reaction of the body to pollen.

CC Sequence 47 AA;

SQ Query Match 22.5%; Score 1.8; DB 1; Length 47;

Best Local Similarity 84.0%; Pred. No. 7.58e-03; Mismatches 2; Indels 1; Gaps 1;

Db 12 KLTSGKIASCRVYDGGIAAVONPASW 35

Qy 55 KLTSGKIASCRVYDGGIAAVONPASW 79

RESULT 3

ID W80347 standard; peptide; 17 AA.

AC W80347;

DT 11-JAN-1999 (first entry)

DE Sugi allergen protein Cryj2 derived epitope for T cells.

KW T cell epitope; sugi allergen proteins cryj1; cryj2; treatment;

KW sugi-pollinosis; allergic reaction; pollen.

OS Synthetic.

PN J1059198-A.

PD 29-SEP-1998.

PF 22-DEC-1997; 353448.

PR 24-DEC-1996; JP-343441.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

(SANY) SANKYO CO LTD.

WPI: 98-577037/49.

PT A linked T cell epitope peptide - used for the treatment of sugi-pollinosis.

PT Sug i-allergen protein Cryj2 derived epitope for T cells.

PT Sug i-allergen proteins cryj1; cryj2; treatment;

PT Sug i-pollinosis; allergic reaction; pollen.

PT Sug i-pollinosis; an allergic reaction of the body to pollen.

PT Sug i-pollinosis; an allergic reaction of the body to pollen.

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PT Sug i-pollinosis; an allergic reaction of the body to pollen.

PT Sug i-pollinosis; an allergic reaction of the body to pollen.

Db 1 FASKNFHQKNGQIAAVONPASKLTSKIAS 31

Qy 34 FASKNFHQKNTG-TG-RRRISLKLTSKIAS 63

RESULT 5

ID R81582 standard; Peptide; 17 AA.

AC R81582;

DT 24-MAY-1996 (first entry)

DE Cedar pollen allergen peptide 10 (T-cell epitope).

KW Cedar; Cryptomeria Japonica; pollen; allergen; immunoglobulin E; IGE; T-cell epitope; antibody; pollinosis; therapy; immunotherapy.

OS Synthetic.

PN EP-70092-A.

PD 13-MAR-1996.

PF 08-SEP-1995; 306295.

PR 10-SEP-1994; JP-242137.

PR 14-JUL-1995; JP-200224.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

Hino K., Saito S., Taniguchi Y;

WPI: 96-14097615.

PT New peptide(s) derived from cedar pollen allergens - activate allergen-specific T-cells, but not allergen-specific IgE antibodies,

PT used for treating cedar pollinosis

PS Claim 4; Page 28; 36PP; English.

CC Synthetic Peptides based on portions of cedar pollen allergens A (R81586) and B (R81587) were tested

CC cedar allergen-specific T-cells, but not allergen-specific IgE antibodies. 6 Peptides (R81580-8185) were identified as T-cell

CC epitopes. These peptides, plus subsequences (R81573-79) essential for T-cell recognition, and homologous peptides (R81588-96) can

CC be used as immunotherapeutic agents to treat or prevent cedar

CC pollinosis, avoiding side-effects such as anaphylaxis.

Sequence 17 AA;

Query Match 20.2%; Score 1.5; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.47e-02; Mismatches 0; Indels 0; Gaps 0;

Db 1 DIFASKNFHQKNTG 17

Qy 32 DIFASKNFHQKNTG 48

RESULT 6

ID W00345 standard; peptide; 17 AA.

AC W00345;

DT 11-JAN-1999 (first entry)

DE Sugi allergen protein Cryj2 derived epitope for T cells.

KW T cell epitope; sugi allergen proteins cryj1; cryj2; treatment;

KW sugi-pollinosis; allergic reaction; pollen.

OS Synthetic.

PN J1059198-A.

PD 29-SEP-1998.

PF 22-DEC-1997; 353448.

PR 24-DEC-1996; JP-343441.

PS Claim 10; Page 5; 21PP; Japanese.

CC W80339-58 represent epitopes for T cells, derived from the sugi allergen proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49 and W80354-55). The peptides are useful for the treatment of sugi-pollinosis, an allergic reaction of the body to pollen.

CC Sequence 33 AA;

Query Match 20.6%; Score 1.7; DB 1; Length 33;

Best Local Similarity 67.7%; Pred. No. 6.45e-02; Mismatches 4; Indels 1; Gaps 1;

Db 1 IDIFASKNFHQKNTG 17

Qy 31 IDIFASKNFHQKNTG 47

RESULT 4

ID W80339 standard; peptide; 33 AA.

AC W80339;

DT 11-JAN-1999 (first entry)

DE Sugi allergen protein Cryj1 derived epitope for T cells.

KW T cell epitope; sugi allergen proteins cryj1; cryj2; treatment;

KW sugi-pollinosis; allergic reaction; pollen.

OS Synthetic.

PN J1059198-A.

PD 29-SEP-1998.

PF 22-DEC-1997; 353448.

PR 24-DEC-1996; JP-343441.

PS Claim 10; Page 5; 21PP; Japanese.

CC W80339-58 represent epitopes for T cells, derived from the sugi allergen proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49 and W80354-55). The peptides are useful for the treatment of sugi-pollinosis, an allergic reaction of the body to pollen.

CC Sequence 33 AA;

Query Match 20.6%; Score 1.7; DB 1; Length 33;

Best Local Similarity 67.7%; Pred. No. 6.45e-02; Mismatches 4; Indels 1; Gaps 1;

Db 1 IDIFASKNFHQKNTG 17

Qy 31 IDIFASKNFHQKNTG 47

		SO	Sequence	15 AA;
Db	1	VDGIIAYQNPASWK	16	:
Qy	65	RVDGIIAYQNPASWK	80	:
RESULT	7			
ID	R81580	standard; Peptide; 17 AA.		
AC	R81580;			
DT	24-MAY-1996	(first entry)		
DE	Cedar pollen allergen peptide 8 (T-cell epitope).			
KW	Cedar; Cryptomeria Japonica; pollen; allergen; immunoglobulin E; IgE; T-cell epitope; antibody; pollinosis; therapy; immunotherapy; OS Synthetic.			
PR	EP-700929-A2.			
PD	13-MAR-1996.			
PF	08-SEP-1995; 306295.			
PR	10-SEP-1994; JP-242137.			
PR	14-JUL-1995; JP-200221.			
PA	(HAYB.) HAYASHIBARA SEIBUTSU KAGAKU.			
PI	Hino K., Saito S., taniguchi Y;			
DR	WPI; 96-140576/15.			
PT	New peptides derived from cedar pollen allergens - activate allergen-specific T-cells, but not allergen-specific IgE antibodies, used for treating cedar pollinosis.			
PS	Claim 4; Page 28; 36pp; English.			
CC	Synthetic Peptides based on portions of cedar pollen allergens A (R81580) and B (R81587) were tested for their ability to activate cedar pollen antigen T-cells, but not allergen-specific IgE antibodies. 6 Peptides (R81580-R81585) were identified as T-cell epitopes. These peptides, plus subsequences (R81573-79) essential for T-cell recognition, and homologous Peptides (R81588-96) can be used as immunotherapeutic agents to treat or prevent cedar pollinosis, avoiding side-effects such as anaphylaxis.			
SQ	17 AA;			
Query Match	19.5%;	Score 111; DB 1; Length 17;		
Best Local Similarity	93.8%;	Pred. No. 2.03e-01; Mismatches 1; Indels 0; Gaps 0;		
Matches	15;	Conservative		
Db	1	KVGDIIAYQNPASWK	16	:
Qy	65	RVDGIIAYQNPASWK	80	:
RESULT	8			
ID	R97884;	standard; peptide; 15 AA.		
AC	R97884;			
DT	16-Aug-1996	(first entry)		
DE	Japan cedar pollen mature allergen Cry J II amino acids 66-80.			
KW	Allergen; epitope; overlapping peptide; Cry J II; cedar pollen; Sugi pollinosis; diagnosis; treatment.			
OS	Cryptomeria Japonica.			
JO804739-A.				
PD	20-FEB-1996.			
PF	07-NOV-1994; 297840.			
PR	05-NOV-1993; JP-278773.			
PR	26-MAY-1994; JP-134868.			
PA	(MEIP-) MEIJI MILK PROD CO LTD.			
DR	WPI; 96-146249/17.			
PT	Japan cedar pollen allergen Cry J II epitope - comprises at least part of specified 460 amino acid protein.			
PS	Claim 3; 1pp; Japanese.			
CC	R97871-897950 are overlapping Peptides used for the epitope mapping of the Japan cedar pollen allergen Cry J II. Cry J II and allergenic peptides of it are useful in the diagnosis, prevention and treatment of Sugi pollinosis the allergic reaction to Japan cedar pollen. Significant regions of the allergen were identified using the overlapping peptides of the full epitope derived from a Cry J II antigen-specific T cell line. Amino acids 66-80 (R97884) and 186-200 (R978908) of the full mature 460 amino acid allergen are the most allergenic of the 90 peptides tested.			
RESULT	9			
ID	W57760;	standard; peptide; 15 AA.		
AC	W57760;			
DT	17-SEP-1998	(first entry)		
DE	Residues 66-80 of Cry J 2.			
KW	HLA class II molecule.			
OS	Cryptomeria Japonica.			
PN	WO820902-A1.			
PD	22-MAY-1998.			
PR	12-NOV-1997; J04129.			
PA	(MEIP-) MEIJI MILK PROD CO LTD.			
PI	Dairiki K., Kino K., Kume A., Sone T;			
DR	WPI; 98-297617/26.			
PT	Peptides derived from Japanese cedar pollen antigens are immunotherapeutic agents - useful for allergy treatment and typing HLA class II molecules in allergy sufferers.			
PS	Claim 12; Page 30; 50pp; Japanese.			
CC	This sequence represents Residues 66-80 of the Cry J 2 protein, and is a peptide of the invention. The peptides are derived from Japanese cedar pollen antigens, and are used as immunotherapeutic agents in the treatment of allergy. The peptides can be used for identification and typing of the particular HLA class II molecules in an allergy sufferer, and also for peptide immunotherapy of an allergy. Using these peptides, the immunotherapy can be targeted more specifically to the requirements of the individual patient, allowing more effective treatment of an allergy. Including those patients for whom treatment with a conventional immunotherapeutic agent is ineffective.			
SQ	15 AA;			
Query Match	18.8%;	Score 107; DB 1; Length 15;		
Best Local Similarity	100.0%;	Pred. No. 4.34e-01; Mismatches 0; Indels 0; Gaps 0;		
Matches	15;	Conservative		
Db	1	VDGIIAYQNPASWK	15	:
Qy	66	VDGIIAYQNPASWK	80	:
RESULT	10			
ID	W80350;	standard; Peptide; 47 AA.		
AC	W80350;			
DT	11-JAN-1999	(first entry)		
DE	Sugi allergen Protein CryJ1 derived epitope for T cells.			
KW	T cell epitope; sugi allergen proteins CryJ1; cryJ2; treatment; sugi-pollinosis; allergic reaction; pollen.			
OS	Synthetic.			
PN	J10250198-A.			
PD	29-SEP-1998.			
PF	22-DEC-1997; 353448.			
PR	24-DEC-1996; JP-343441.			
PA	(HAYB.) HAYASHIBARA SEIBUTSU KAGAKU.			
DA	(SANYO) SANKYO CO LTD.			
DR	WPI; 98-570374/9.			
PT	A linked T cell epitope peptide - used for the treatment of sugi-pollinosis.			
CC	Claim 10; Page 5; 21pp; Japanese.			
CC	W8039-58 represent epitopes for T cells, derived from the sugi allergen proteins CryJ1 (W80339-44, W80350-53 and W80355-58) and CryJ2 (W803345-49 and W80355-55). The peptides are useful for the treatment of sugi-pollinosis, an allergic reaction of the body to pollen.			

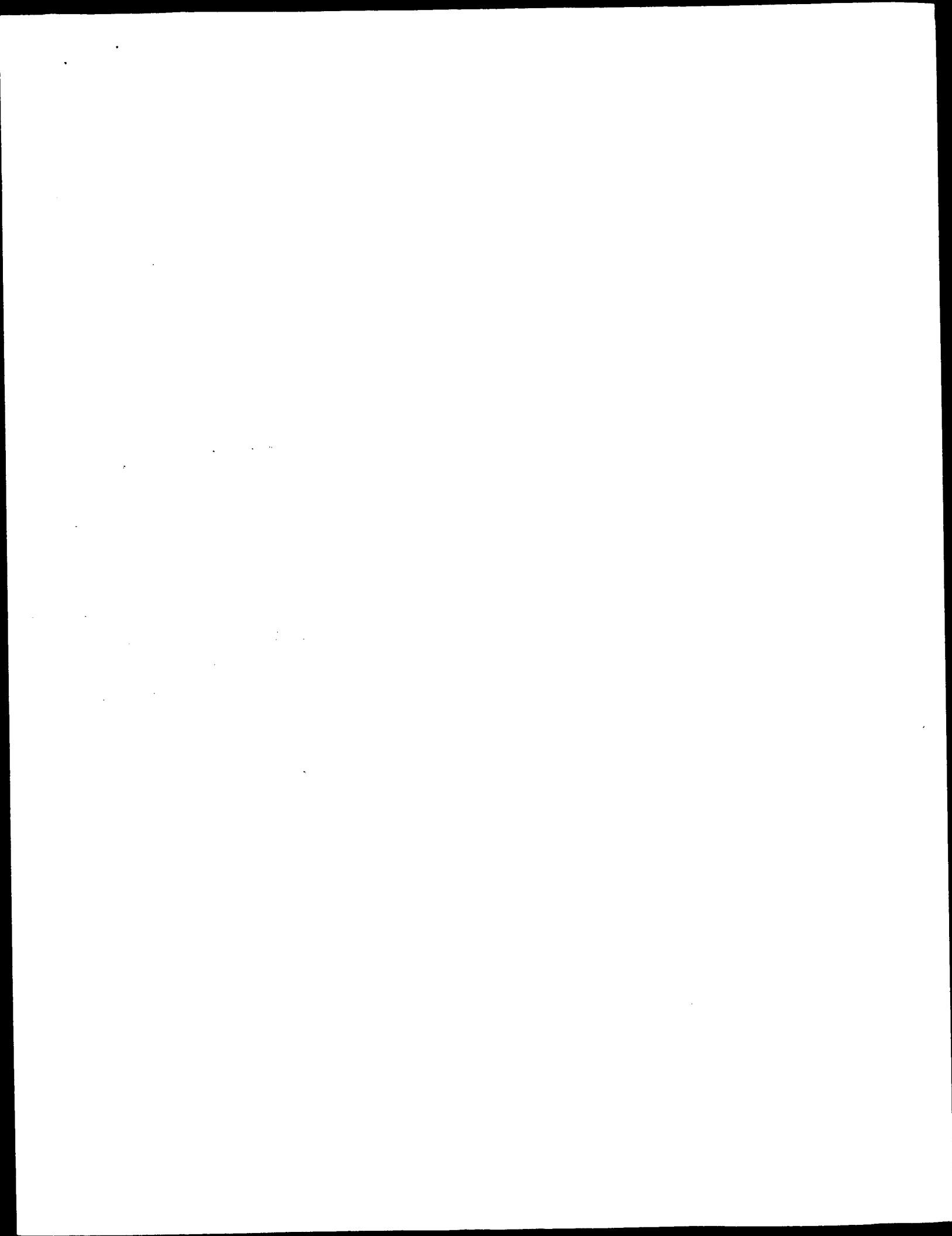
Query Match 17.2%; Score 98; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.33e+00; Matches 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0;
 Db 1 ASKNFHLQKNITGTG 15
 Oy ||||||| 35 ASKNFHLQKNITGTG 49

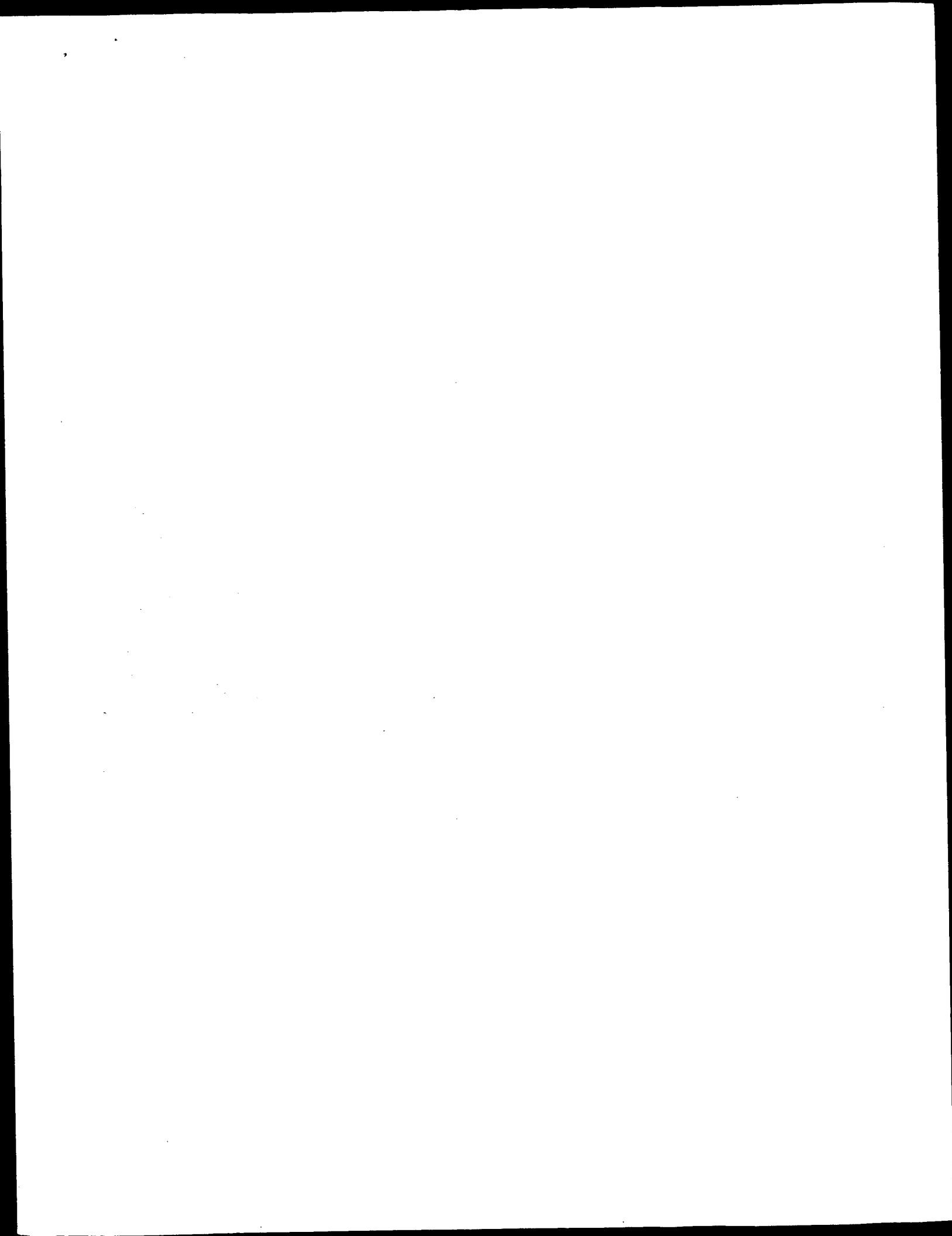
RESULT 15
 ID R97907 standard; peptide: 15 AA.
 AC R97907;
 DT 16-Aug-1996 (first entry)
 DE Japan cedar pollen mature allergen Cry j II amino acids 181-195.
 KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
 Sugi pollinosis; diagnosis; treatment.
 OS Cryptomeria japonica.
 PN J0807392-A.
 PD 20-FEB-1986.
 PP 07-NOV-1994; 297840.
 PR 05-NOV-1993; JP-276773.
 26-MAY-1994; JP-134868.
 PA (MEIP) MEIJI MILK PROD CO LTD.
 DR WPI: 95-166249/17.
 PT Japan cedar pollen allergen Cry j II epitope - comprises at least
 PT part of specified 460 amino acid protein
 PS Claim 8; Fig 4; Japanese.
 CC R9781-R97960 are overlapping peptides used for the epitope mapping
 of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
 peptides of it are useful in the diagnosis, prevention and treatment
 of Sugi pollinosis, the allergic reaction to Japan cedar pollen.
 Significant regions of the allergen were identified using the
 overlapping peptides of the full epitope derived from a Cry j II
 antigen specific T cell line. Amino acids 66-80 (R97884) and 186-200
 (R97908) of the full mature 460 amino acid allergen are the most
 allergenic of the 90 peptides tested.
 SQ Sequence 15 AA;

Query Match 17.2%; Score 98; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.33e+00; Matches 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0;

Db 2	IDFASKNFHLQKN 15
Oy	31 IDFASKNFHLQKN 44

Search completed: Mon Jun 19 15:57:41 2000
 Job time : 14 secs.





Page 1

This block contains five dashed outlines of Chinese characters arranged vertically: 人, 田, 五, 九, and 一. Each character is enclosed in a dashed rectangular frame for tracing practice. To the right of the characters is a decorative vertical border consisting of a series of small, stylized star-like symbols.

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MARCH 22, 1945

Mon Jun 19 15:55:43 2000 : Masdar time = 55 seconds

tabular output not generated.

Title: >US-09-142-524A-1
Description: (1-80) from NS0014252A1, 2000

perfect score: 569 sequence: 1 MKVTVAFNQFGPNRRVFIKR . . . TASRRVDTIAVNQDASHW 80

Scoring table: PAM 150 Gen 11

searched: 83857 seeds, 30454973 residues

Post-processing: Minimum Match 0%

Maximum DB seq length 80

1:swissprot

Statistics: Mean 40.706; Variance 73.263; scale 0.556

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

2

SUMMARIES

Score

ON DATA MOTION

search completed: Mon Jun 18 15:56:03 2000

